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Abstract

Intestinal helminth infections cause health and welfare problems in both human and animal populations. Heritability analysis of a resource population of pigs infected with *Ascaris suum* (large roundworm) and *Trichuris suis* (whipworm) has shown high heritabilities for parasite burdens of both parasites. A number of putative QTL regions have been identified through a genome scan using a 7K porcine SNP-chip. To validate a QTL associated with *Ascaris* worm load on SSC4, we have genotyped two of the most promising SSC4 candidates in another population consisting of 174 pigs from 39 litters infected with *Ascaris*. The population used for the validation was produced by sows inseminated with mixed semen from three boars. The heritability (±SE) of worm burden of non-larval *Ascaris* (>2cm), adult *Ascaris* (>10cm), and total number of *Ascaris* was 73.1% (±0.17), 31.4% (±0.15), and 36.9% (±0.16), respectively. The two SSC4 SNPs were genotyped using the TaqMan SNP Genotyping Assay. One SNP was associated with both adult *Ascaris* burden ($P<0.001$) and total *Ascaris* burden ($P<0.01$). Future research will further investigate this QTL associated with *Ascaris* burden.